SEQUENCE LISTING

<110> Weterings, Koen
      Apuya, Nestor R.
      Tatarinova, Tatiana
      Goldberg, Robert B.
      The Regents of the University of California

<120> Polynucleotides Useful for Modulating Transcription

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<140> US 09/724,857
<141> 2000-11-28

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<170> PatentIn Ver. 2.1

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atatttgtta ataaaaatac tttgagctct tcttcataag acttttccag cttccatcta   3540

gaaaatcaca taaattaaaa gataaataac cgaataaaca tagttcacat tctaactctt    3600

agtcttagat ttgttttaat tttcaaaggt ttaggtattg tatatgtttt ttttattggg   3660

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tcaaaacaaa agttaaagca gac atg aag caa cag caa cgt tac ttg gtc       5510
                          Met Lys Gln Gln Gln Arg Tyr Leu Val
                           1                   5
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9

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gtc ttc atc gtc ctt tta agc ttt ctt ctg gtaaagcttc ttccttaatt          5560
Val Phe Ile Val Leu Leu Ser Phe Leu Leu.
 10                  15

atattaaaac cctaattaag atctcatata tctgaatgtt gtatatattt gttggtatag      5620

ttt gtg aat ctg agt gaa gga aga aca gga gga gtt gca gaa gaa tat        5668
Phe Val Asn Leu Ser Glu Gly Arg Thr Gly Gly Val Ala Glu Glu Tyr
 20                  25                  30                  35

tgg aag aag atg atg aag aat gaa ccg ttg cct gaa cca atc aaa gag        5716
Trp Lys Lys Met Met Lys Asn Glu Pro Leu Pro Glu Pro Ile Lys Glu
                40                  45                  50

ctt ctc aac aat cct ttt agg acc gca caa gag aga ttc atc cag aat        5764
Leu Leu Asn Asn Pro Phe Arg Thr Ala Gln Glu Arg Phe Ile Gln Asn
                55                  60                  65

ttc gac acc aaa tct gtt gtc atc atc tac cac aat cct aat gaa taa       5812
Phe Asp Thr Lys Ser Val Val Ile Ile Tyr His Asn Pro Asn Glu
                70                  75                  80

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tatacacgta tactaaatat gttctgttta gtgcagaaat gttaacccta gctataaggg      5992

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aattagattt gcttcacatt ttgttttgat atatataaat caatatactg tgcctttcgt      6112

gtcttgtttc ttatattatt ttgtgacatt aattaattat cttatcaaaa atttatttta      6172

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<213> Arabidopsis thaliana

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<223> Arabidopsis G654

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                20                  25                  30
Glu Glu Tyr Trp Lys Lys Met Met Lys Asn Glu Pro Leu Pro Glu Pro
            35                  40                  45
Ile Lys Glu Leu Leu Asn Asn Pro Phe Arg Thr Ala Gln Glu Arg Phe
                50                  55                  60
Ile Gln Asn Phe Asp Thr Lys Ser Val Val Ile Ile Tyr His Asn Pro
 65                  70                  75                  80
Asn Glu
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10

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<212> DNA
<213> Phaseolus coccineus

<220>
<223> Scarlet Runner Bean C541 genomic region

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<221> CDS
<222> (3154)..(3552)
<223> Scarlet Runner Bean C541

<220>
<221> modified_base
<222> (1)..(4846)
<223> n = g, a, c or t

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acttgaggat atagtctcct gaaccagctg tcacggctga gttagataac attactgaat 180

ttctacggga gcggttgaaa tcactttcgc ccctttaaga agaagcctac accgggcacc 240

ttctttacgc aattcgaaat ttagtcttgc caggcagtcg ttggatcgaa ggtctttttc 300

gataccgagg aatctgactt tgcaaggaat aattcctaat cacaccaccc caacccctga 360

atacacttca ggaccctctg aaaccaactt cgtttcggct aaatcacaag aatctcccac 420

tcattccgat .tttagccaat aaatatgat atcggtctgg gaagccgata aggaaattct 480

acaaaaagag tttatgaatg aggaaaataa ggaaaagaga gaactatttt ttaggtaccc 540

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gaatatccnn nnnaatggtt agataatata agaaaaggat aagtatgatt aaactgaaac 660

cacgtcggca gaaacaaagt gaattccccc ctttagagga agttcgtttc ttaaatatag 720

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taaaagatat tcaaaatcta cacagtcaac taaattttac taatcaaatg cttttttcaat 840

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ttaaattctc agaagaagag ataaaacagt taaaaattgg tcaaactttg gattctttat 960

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atgatatgcc caaaaggaca aatccaaatc aagaagtttt agacgaaatc gaaagagat 1080

taaaacaaac tctgaacgac acaataaatg tgatagaaga aactaaaaac tcagactcat 1140

gttcagagtc tcccgatcgt attgaaaaaa taaaacgtaa taaatcagag atttccagta 1200

agccgaaatt tttacactcg ccccaccttc gatatcatcg agatggcgat ggacacctca 1260

11

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aaaattaatt atatctggat tcacgggagt attaaaaggc tggtgggata attacctcat 1440

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gaagaatcaa taggagattc tgattacgaa gtattggaca tgaggataac aattgtaatt 2280

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12

taaagaaaaa aggttgagaa aggtgcagca aca atg tct cca ttc tgt aga aac 3174
                                      Met Ser Pro Phe Cys Arg Asn
                                       1   5

ttt tca atg gca tgg gtg ctt atg gca ttt gtg ttg ttt gca aac agt 3222
Phe Ser Met Ala Trp Val Leu Met Ala Phe Val Leu Phe Ala Asn Ser
        10   15   20

gct atg ccc aca aat gga tcc act gtt ggg gta aaa aac atg ttg ggt 3270
Ala Met Pro Thr Asn Gly Ser Thr Val Gly Val Lys Asn Met Leu Gly
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ggt aaa ttg atg cta aac gtt tta tgt ccc cat att gat aag caa cac 3318
Gly Lys Leu Met Leu Asn Val Leu Cys Pro His Ile Asp Lys Gln His
40   45   50   55

att atc ccg aat ggt ggt tca ttt gag tgg aag tac aat ggt ggt gct 3366
Ile Ile Pro Asn Gly Gly Ser Phe Glu Trp Lys Tyr Asn Gly Gly Ala
            60   65   70

cca cca ata gga caa tca cca ttc atg tgt ttc ttt cgg tgg aat aat 3414
Pro Pro Ile Gly Gln Ser Pro Phe Met Cys Phe Phe Arg Trp Asn Asn
            75   80   85

gtt cat cac tcc ctt gat ctg tgt tca cca agc aag tat act ggt tgt 3462
Val His His Ser Leu Asp Leu Cys Ser Pro Ser Lys Tyr Thr Gly Cys
        90   95   100

gaa aat gcc att tgg gaa atc aaa gaa aag caa ttt tgt agg tac aga 3510
Glu Asn Ala Ile Trp Glu Ile Lys Glu Lys Gln Phe Cys Arg Tyr Arg
105   110   115

ggt gga cct att aat tat ttt tgc tat gac tgg gat gat tag 3552
Gly Gly Pro Ile Asn Tyr Phe Cys Tyr Asp Trp Asp Asp
120   125   130

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aaagtctttc agaccctctg acacatgtat catctgctcg tatatgtgat acagtcatcg 4212

cagttcacaa gataacaaga aaaccaaggg taagctaatg aaaaaaaatt ccataacata 4272

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13

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gttatataaa atttcaatat caatttcatc attcatatag accacacatg gatctatttt  4392

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atgcccctac cagagactaa cacctaatca aagagaaatg atcaaggtaa gttcaaacat  4512

ccaataacga gtgcctacag tgggacccaa tgtgtatgaa ctccttatca gcttctcacc  4572

acctgatatc ttattctata tgacgtagat catcagtgaa actagaggat ctccgttaaa  4632

catatgtttt ttatacttaa tgtcatcaaa caacaactca cacattatcc caaatgtatg  4692

acatcaattt catacaattt tcatcattca tatataatac atatcattga atcacataac  4752

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<210> 7
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<212> PRT
<213> Phaseolus coccineus

<220>
<223> Scarlet Runner Bean C541

<400> 7

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Phe Val Leu Phe Ala Asn Ser Ala Met Pro Thr Asn Gly Ser Thr Val
                20                  25                  30
Gly Val Lys Asn Met Leu Gly Gly Lys Leu Met Leu Asn Val Leu Cys
            35                  40                  45
Pro His Ile Asp Lys Gln His Ile Ile Pro Asn Gly Gly Ser Phe Glu
        50                  55                  60
Trp Lys Tyr Asn Gly Gly Ala Pro Pro Ile Gly Gln Ser Pro Phe Met
65                  70                  75                  80
Cys Phe Phe Arg Trp Asn Asn Val His His Ser Leu Asp Leu Cys Ser
                85                  90                  95
Pro Ser Lys Tyr Thr Gly Cys Glu Asn Ala Ile Trp Glu Ile Lys Glu
                100                 105                 110
Lys Gln Phe Cys Arg Tyr Arg Gly Gly Pro Ile Asn Tyr Phe Cys Tyr
            115                 120                 125
Asp Trp Asp Asp
        130
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<210> 8
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<212> DNA
<213> Arabidopsis thaliana

<220>
<223> Arabidopsis C541 genomic region

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<222> (1693)..(2178)
<223> Arabidopsis C541
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aatcaaaaaa gttgttatat ggtacatggc acaatcttat aaattattaa tttgaaaacg 180

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aacaaatcaa gtaaagttgg gcacctcaat tgttttaaaa aagtttgggt acctcaaaaa 420

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cacagtatat aactcattcg acatttacaa acaacattgt gctagcttaa actccctctc 1680

ctattcaaaa aa atg gat att cca aag caa tat cta tca cta ttc ata ttg 1731
                Met Asp Ile Pro Lys Gln Tyr Leu Ser Leu Phe Ile Leu
                 1               5                    10
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15

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att atc ttc ata act aca aaa tta tca caa gcc gac cat aaa aac gac    1779
Ile Ile Phe Ile Thr Thr Lys Leu Ser Gln Ala Asp His Lys Asn Asp
     15                  20                  25

att cca gtt ccc aac gat cca tca tca aca aat tct gtg ttt cct acc    1827
Ile Pro Val Pro Asn Asp Pro Ser Ser Thr Asn Ser Val Phe Pro Thr
 30                  35                  40                  45

tcg aaa aga acc gtg gaa atc aat aat gat ctc ggt aat cag cta acg    1875
Ser Lys Arg Thr Val Glu Ile Asn Asn Asp Leu Gly Asn Gln Leu Thr
             50                  55                  60

tta ctg tat cat tgt aaa tca aaa gac gat gat tta ggt aac cgg act    1923
Leu Leu Tyr His Cys Lys Ser Lys Asp Asp Asp Leu Gly Asn Arg Thr
             65                  70                  75

ctg caa cca ggt gag tcg tgg tct ttt agt ttc ggg cgt caa ttc ttt    1971
Leu Gln Pro Gly Glu Ser Trp Ser Phe Ser Phe Gly Arg Gln Phe Phe
             80                  85                  90

gga agg acg ttg tat ttt tgt agt ttt agt tgg cca aat gaa tcg cat    2019
Gly Arg Thr Leu Tyr Phe Cys Ser Phe Ser Trp Pro Asn Glu Ser His
     95                  100                 105

tcg ttc gat ata tat aaa gac cat cga gat agc ggc ggt gat aac aag    2067
Ser Phe Asp Ile Tyr Lys Asp His Arg Asp Ser Gly Gly Asp Asn Lys
110                  115                 120                 125

tgc gag agc gac agg tgt gtg tgg aag ata aga aga aac gga cct tgt    2115
Cys Glu Ser Asp Arg Cys Val Trp Lys Ile Arg Arg Asn Gly Pro Cys
                 130                 135                 140

agg ttt aac gat gaa acg aag cag ttt gat ctt tgt tat cct tgg aat    2163
Arg Phe Asn Asp Glu Thr Lys Gln Phe Asp Leu Cys Tyr Pro Trp Asn
             145                 150                 155

aaa tct ttg tat tga caacaatatg ctgatgttct gtcttttacg actcatggag    2218
Lys Ser Leu Tyr
         160


tttcattgtt tgaaacaata atataaaaca tataaaattt ctattattcc aagttccaac 2278

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16

<220>
<223> Arabidopsis C541

<400> 9
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             20                  25                  30
Pro Asn Asp Pro Ser Ser Thr Asn Ser Val Phe Pro Thr Ser Lys Arg
             35                  40                  45
Thr Val Glu Ile Asn Asn Asp Leu Gly Asn Gln Leu Thr Leu Leu Tyr
         50                  55                  60
His Cys Lys Ser Lys Asp Asp Asp Leu Gly Asn Arg Thr Leu Gln Pro
 65                  70                  75                      80
Gly Glu Ser Trp Ser Phe Ser Phe Gly Arg Gln Phe Phe Gly Arg Thr
                 85                  90                      95
Leu Tyr Phe Cys Ser Phe Ser Trp Pro Asn Glu Ser His Ser Phe Asp
            100                 105                 110
Ile Tyr Lys Asp His Arg Asp Ser Gly Gly Asp Asn Lys Cys Glu Ser
            115                 120                 125
Asp Arg Cys Val Trp Lys Ile Arg Arg Asn Gly Pro Cys Arg Phe Asn
    130                 135                 140
Asp Glu Thr Lys Gln Phe Asp Leu Cys Tyr Pro Trp Asn Lys Ser Leu
145                 150                 155                     160
Tyr
```

<210> 10
<211> 10
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:promoter
      control region homologous repeat of Scarlet
      Runner Bean G564 and C541 promoter region

<400> 10
gaaaagcgaa   10

<210> 11
<211> 10
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:promoter
      control element homologous repeat of Scarlet
      Runner Bean G564 promoter region

<400> 11
gaaaagtgaa   10

<210> 12
<211> 10
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:promoter
      control element of Arabidopsis G564 ortholog
      promoter region

<400> 12
gaaaagccaa   10

<210> 13
<211> 450
<212> DNA
<213> Phaseolus coccineus

<220>
<223> Scarlet Runner Bean G564 promoter (-921 to -662)
      PLACE database Signal Scan search sequence

<400> 13
tgaaaagtga agaaaaccat gtaatgaaaa caaaatggca cgacaatcaa aaaaagtttt 60
cacgcaaaat tttcttcaaa atttataaca ttttcatgtt gtgtttgttt caaagcctag 120
aaaaacgaag agttactatt ggtaatgaaa agcgaagaaa accacataat aaaaacaaaa 180
tggcacgaca atcaagaaaa agttttcaca caaactttt ttcaaaattt actatgttta 240
tttcgaaatt tagaaaaacg aagagttatt attagtaatg aaaagcgaag aaaactacgt 300
cagaaagtta tatatattaa ttaattaatt ttcatttact tttttccctt tttattttaa 360
agttaaatta ttattatttt catttaaaat   420
                                                                    450

<210> 14
<211> 448
<212> DNA
<213> Phaseolus coccineus

<220>
<223> Scarlet Runner Bean G564 promoter (-921 to -662)
      PlantCARE database Signal Scan search sequence

<400> 14
gaaaagtgaa gaaaaccatg taatgaaaac aaaatggcac gacaatcaaa aaaagttttc 60
acgcaaaatt ttcttcaaaa tttataacat tttcatgttg tgtttgtttc aaagcctaga 120
aaaacgaaga gttactattg gtaatgaaaa gcgaagaaaa ccacataata aaaacaaaat 180
ggcacgacaa tcaagaaaaa gttttcacac aaaacttttt tcaaaattta ctatgtttat 240
ttcgaaattt agaaaaacga agagttatta ttagtaatga aaagcgaaga aaactacgta 300
ataaaaaaca aaatggcacg acaataaaaa aagttttcac gcaaaatttt cttggtgcgc 360
agaaagttat atatattaat taattaattt tcatttactt ttttcccttt ttattttaaa 420
gttaaattat tattattttc atttaaaa   448

<210> 15
<211> 10
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:site #S000067
      MARTBOX signal sequence promoter control element

<400> 15
ttwtwttwtt   10

18

```
<210> 16
<211> 10
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:3-AF1 binding
      site promoter control element

<400> 16
aagagttatt                                          10


<210> 17
<211> 10
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Hordeum vulgare
      ABRE and Petroselinum crispum ACE promoter control
      element

<400> 17
actacgtaat                                          10


<210> 18
<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Solanum
      tuberosum AT1-motif promoter control element

<400> 18
ttttattta aa                                        12


<210> 19
<211> 10
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:TC-rich repeat
      promoter control element

<400> 19
gttttcttca                                          10


<210> 20
<211> 10
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:TC-rich repeat
      promoter control element
```

```
<400> 20
attttcttca
```
<div align="right">10</div>

```
<210> 21
<211> 10
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:TC-rich repeat
      promoter control element

<400> 21
gttttcttcg
```
<div align="right">10</div>

```
<210> 22
<211> 10
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:TC-rich repeat
      promoter control element

<400> 22
tttttcttga
```
<div align="right">10</div>

```
<210> 23
<211> 10
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:TC-rich repeat
      promoter control element

<400> 23
tttttctaaa
```
<div align="right">10</div>

```
<210> 24
<211> 10
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:TC-rich repeat
      promoter control element

<400> 24
attttcttgg
```
<div align="right">10</div>

```
<210> 25
<211> 50
<212> DNA
<213> Artificial Sequence
```

<220>
<223> Description of Artificial Sequence:oligonucleotide
     linker-primer

<400> 25
gagagagaga gagagagaga actagtctcg agttttttttt ttttttttt   50

<210> 26
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:anchor/reverse
     primer G primer

<400> 26
aagctttttt tttttg
                                                                          16

<210> 27
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:anchor/reverse
     primer C primer

<400> 27
aagctttttt tttttc
                                                                          16

<210> 28
<211> 13
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:H-AP49 forward
     primer

<400> 28
aagctttagt cca
                                                                          13

<210> 29
<211> 13
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:H-AP50 forward
     primer

<400> 29
aagctttgag act
                                                                          13

<210> 30
<211> 13
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:H-AP51 forward
      primer

<400> 30
aagcttcgaa atg

13

<210> 31
<211> 13
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:H-AP52 forward
      primer

<400> 31
aagcttgacc ttt

13

<210> 32
<211> 13
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:H-AP53 forward
      primer

<400> 32
aagcttcctc tat

13

<210> 33
<211> 13
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:H-AP54 forward
      primer

<400> 33
aagcttttga ggt

13

<210> 34
<211> 13
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:H-AP55 forward
      primer

<400> 34
aagcttacgt tag

<210> 35
<211> 13
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:H-AP56 forward
     primer

<400> 35
aagcttatga agg

<210> 36
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:oligo(dT-20)
     primer

<400> 36
tttttttttt tttttttttt

<210> 37
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:dT-20dN primer

<220>
<221> modified_base
<222> (21)
<223> n = g, c, a or t

<400> 37
tttttttttt tttttttttt n

<210> 38
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:mutagenic oligo

<400> 38
attggactgc atgcttacgc tagtctgtgc agag